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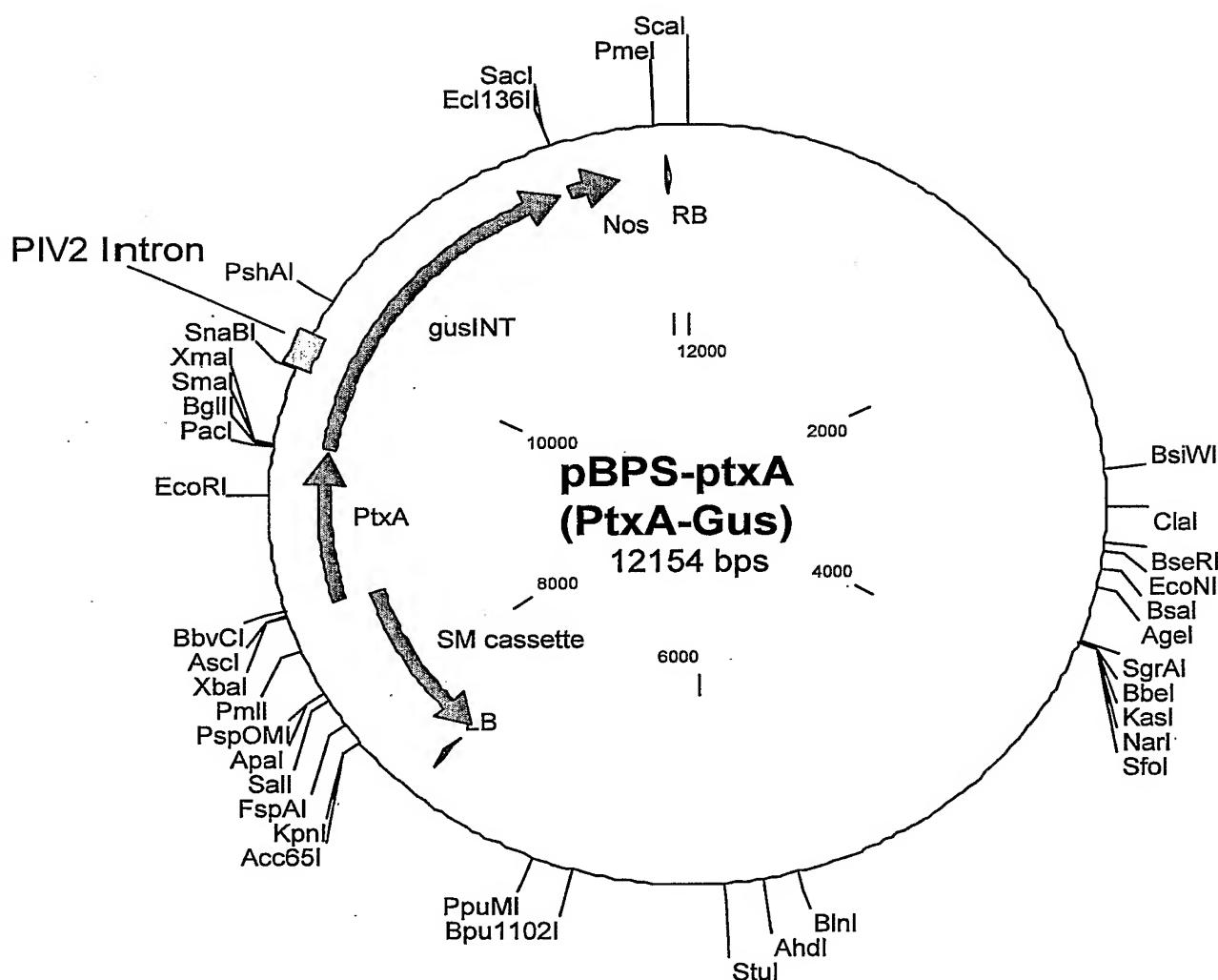


Fig. 1

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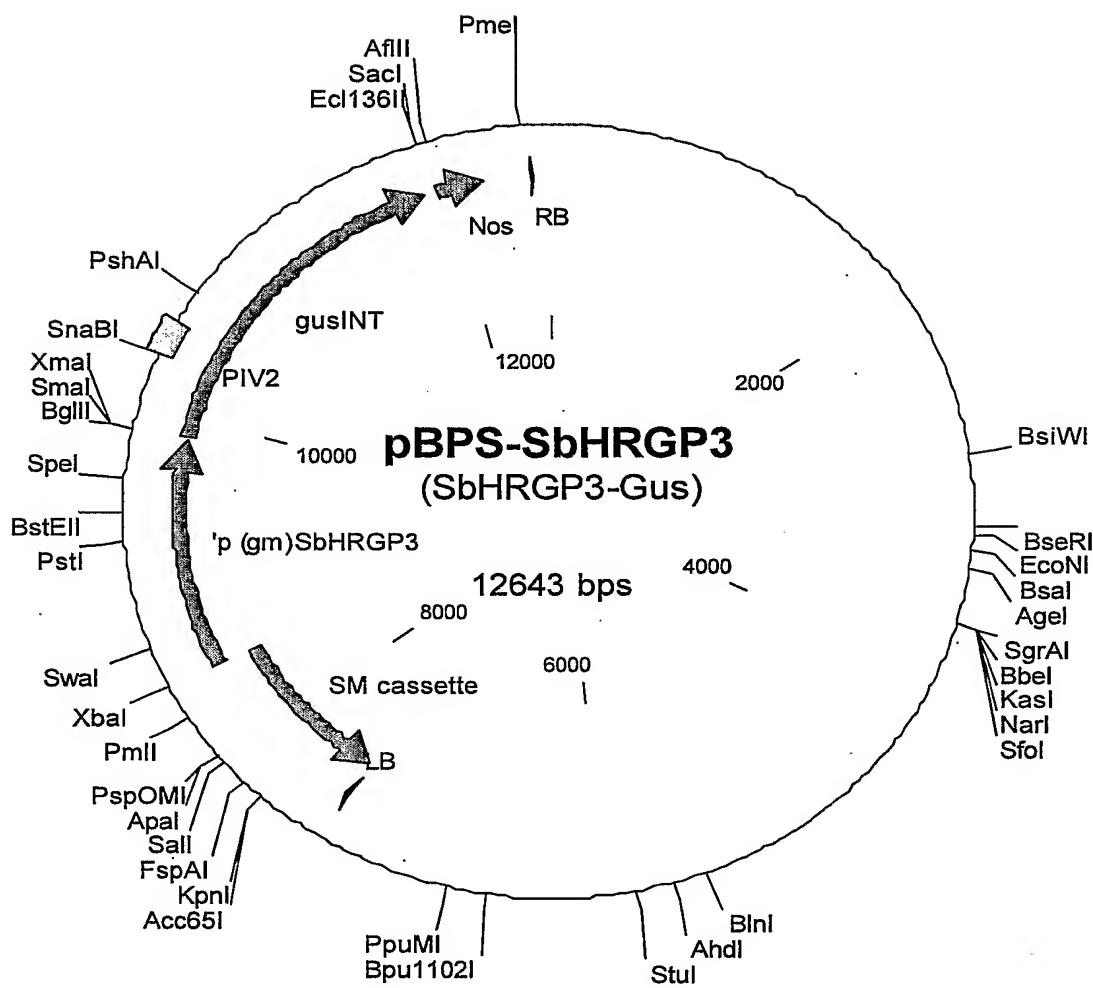


Fig. 2

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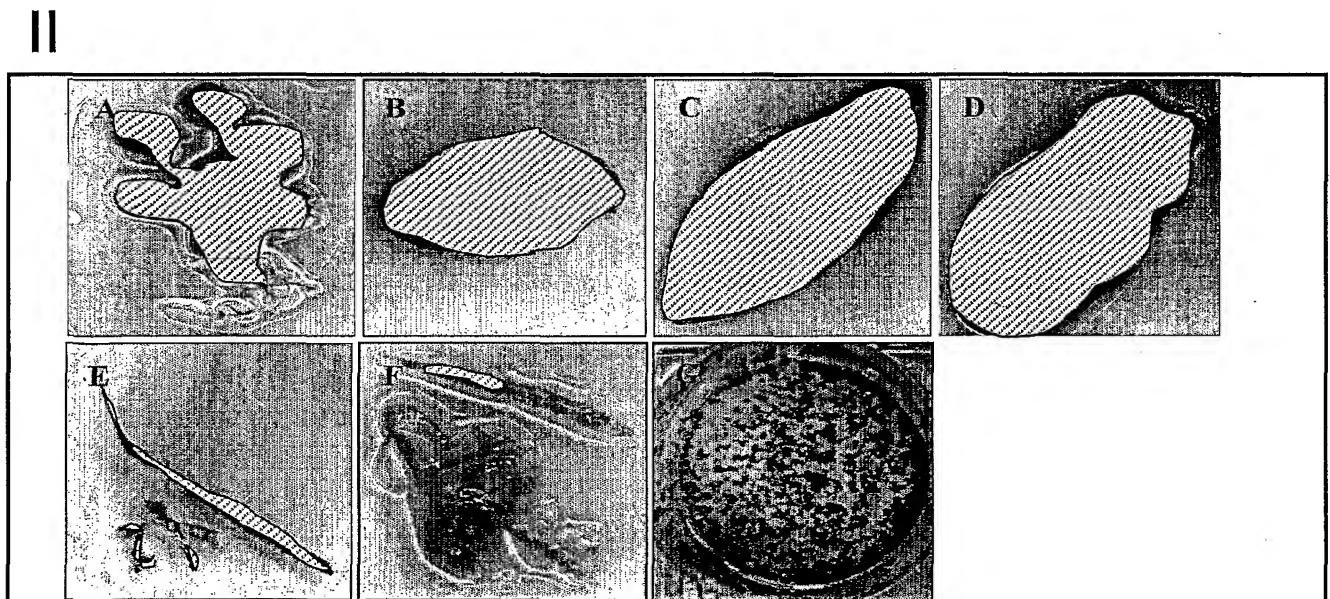
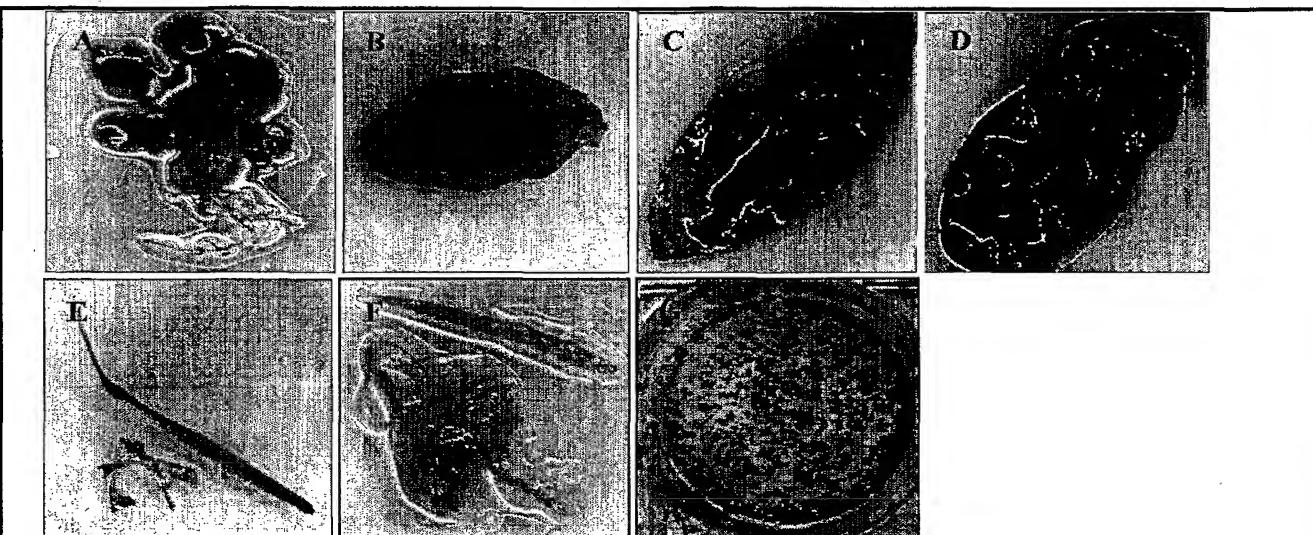


Fig 3

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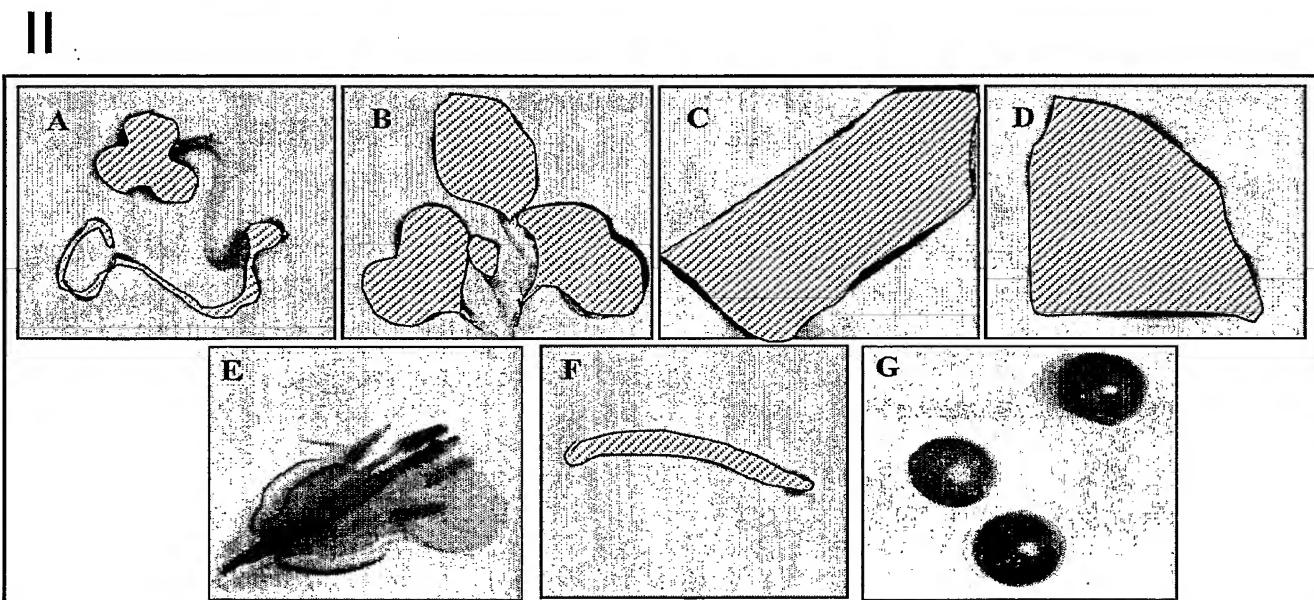
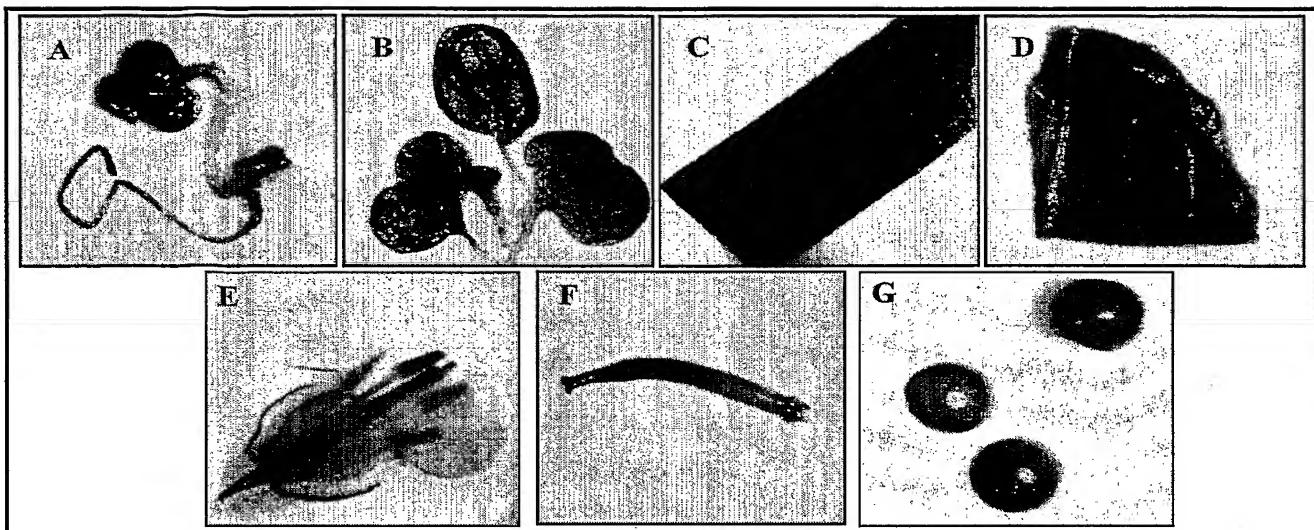
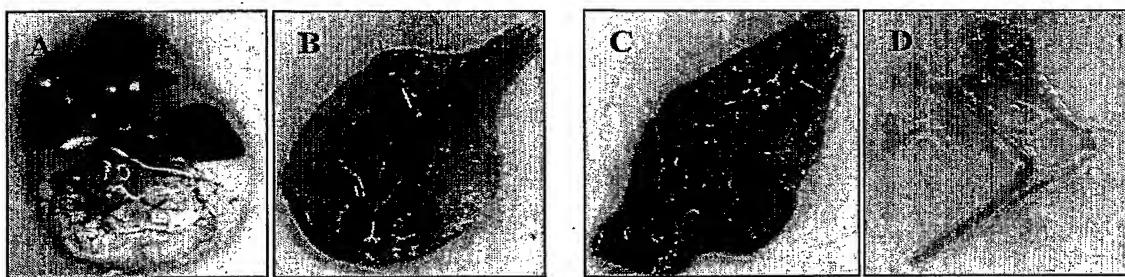


Fig 4

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I



II

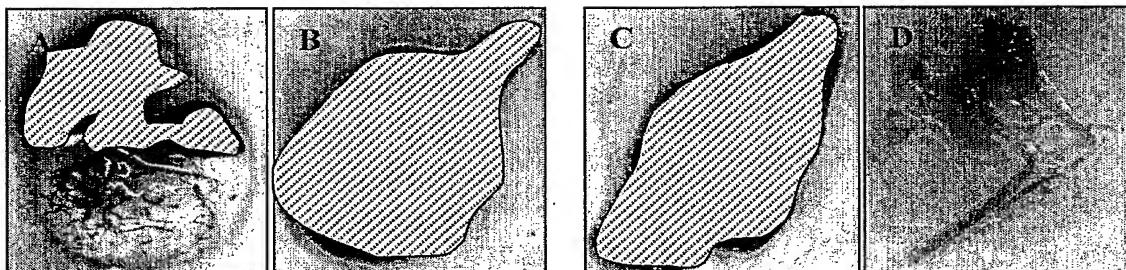


Fig 5

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	1	50
A	(1) MANFAIANVLILLLNLSTLLNLACPYCPYPSPKPPTHKPPIVKPPVHK-	
B	(1) MANYALANVFILLNLSTLLNLIVLACPYCPYPSPKPPTHHPPIVKPPVHKR	
C	(1) -----	
D	(1) -PHVKPPSTPKHPKDPPHVVKPPSTPKQPPYVKPPTPKHPPHVKKPS---	
E	(1) MGKHGLATWLVILLNFATLLTSACSYCPSPSPP-----	
F	(1) MGSRVLASFFVFLIFTVITLPPTIQACTPCTRPHPPVPKP-----	
Consensus	(1) MA ALAS ILLN STLL LAC YCPYPSP PP PP VKPP	
	51	100
A	(50) -----PPKPQPCPPPSSSPKPPHVKPPPHPKPPAVHP	
B	(51) RKYSPTPKPPVHKPPRYPPKSPCPCPPSSTPKPPHVKPPPHPKPPVHP	
C	(1) -----RAESART	
D	(47) -----TPKHPKHP-----QKPCPPPSHHGPKPPIVKP	
E	(35) -----KPP-----KVKHPLPLPPKHPHVKP	
F	(41) -----PQHGGGGGGGSKPPPHGGKGKGKPP	
Consensus	(51) PK PP K PH PPP H PKPP VKP	
	101	150
A	(83) PHVPKPP-AVHPPHVKPPVVHPIVHPPYVPK-----PPVVKPP-----	
B	(101) PHVPKP--PVHPPYVPKPIVVKPIVHPPYVPK-----PPVVKPPPYVPK	
C	(8) HHMFQP---HPP-YVPKPIVVKPIVHPPYVPK-----PPVVKPP-----	
D	(75) PHVPRPP-IVHPPPIVSPPSTPKPPKTPPKPPSIPPIVSP-----	
E	(57) PHTPMP-----PNPPAVKPPYVPK-----PPVVEPP-----	
F	(67) PHGGKGKGPPHHGGGGGGGSPPVVRPPPVVVRP---PPIIRPP-----	
Consensus	(101) PHVPKP VHPPYVPKPIV PPIVHPPYVPK PPVVKPP	
	151	200
A	(122) --VVKPPHVPKPPVVPTPPYIPKPPIVFPFHVKPLPP--VVPVTPPYVPK	
B	(144) PPVVRPPYVPKPPVVPTPPYVPKPPVVRPPYVPKPP--VVPVTPPYVPK	
C	(44) -----PYVPKPPVVRPPYVPKPP--VVPVTPPYVLS	
D	(119) -----IVYPPITPTPPIVHPPVTPKPPSPTPPIVSPPIVY	
E	(83) -----YVPKPPVVKPPYVPKPP--PVVEPPYMP	
F	(109) -----PVVYPPPIVRPPPITRPPIIIPIQPPPVT	
Consensus	(151) V PPYVPKPPPIVRPPYVPKPP VVPVTPPYVLS	
	201	250
A	(168) P-----PIVFPPHVPLPPVVPTPPYVP-----KPIVFPFHVKPLPPVPP	
B	(192) PPIVKPPIVFPPHVPLPPVVPSPPYVPSPPPIVKPPIVFPPHVPLPPVPP	
C	(73) HHCFP-TTVSTSSCTITTLCTNTPIVN-----HQLFFHHMFFYLPVVP	
D	(154) PPITPTPPVVSPIIPTPPIVSPPFVPP-----PPVVP	
E	(108) -----	
F	(140) PPGLLPPITTPPG--LLPPVTTPPGLLP-----PVTTPPG	
Consensus	(201) PP PIV PP V L P V SPPPIVP I F PL PVVP	
	251	300
A	(208) VTPPYVPLPPVVPTPPFVPTPPIITPPTPTVVPVSPPPSETCPFFFFPTV	
B	(242) VTPPYVQPP---PIVTPPTPTPPIVTPPVVSPPTP--PSETPCPPPLVP	
C	(116) VTPPYVQPT-----TYCNSTNTNTSNWTPPTP--PSETLVLPPPLVP	
D	(186) IPPPYVPSP-----PVVTPPIVPTPPTPCPP-----PPPPPAI	
E	(108) -----H	
F	(173) LLPIIINPP-----PVTVPPPSSGYPPYG-----PPSGG	
Consensus	(251) VTPPYVQPP P IV PP TPPTP PSET PPPP	

Fig. 6a

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	301	350
A	(258) VPYPPPAQPTCSIDALKGACVDVLGGLIHIGIGGSAKQTCCPLLQGLVD	
B	(287) YPPTPPAQQTCSIDALKGACVDVLGGLIHIGIGGSAKQTCCPLLQGLVD	
C	(156) YP-PPPAQQTCSIDALKGACVDVLGGLIHIGIGGSAKQTCCPLLQGLVD	
D	(219) IP-SPPAQPTCPIDALKGACVDVLGGLIHIGIGGSAKQTCCPLLGGI	VD
E	(109) DT-----L---KLGACVDLLGGLVHIGIGGSSAKDTCCPVLQGLVD	
F	(202) GGGGGGKQPTCPINALKGACVDVLGGLIHIGLGNPVENVCCPVLQGLLE	
Consensus	(301) P PPAQPTCSIDALKGACVDVLGGLIHIGIGGSAKQTCCPLLQGLVD	
	351	397
A	(308) LDAAVCLCTTIRLKLLNINLVIPLALQVLID-CGKTPPEGFKCPSS-	
B	(337) LDAAICLCTTIRLKLLNINLVIPLALQVLID-CGKTPPEGFKCPAY-	
C	(205) LDAAICLCTTIRLKLLNINLVIPLALQVLID-CGKTPPEGFKCPAS-	
D	(268) LDAAICLCTTIRLKLLNINIIILPIALQVLIDDCGKYPPKDFKCPST-	
E	(146) LDAAVCLCTAIKVVKLLNVNIIIPIALQVLVG-CGKTPPSGFQCPA--	
F	(252) LEAAVCLCTTIRLKLLNINIFIPLALQALIT-CGINPPSGFVCPPLT	
Consensus	(351) LDAAICLCTTIRLKLLNINIVIPLALQVLID CGKTPPEGFKCPAS	

Fig. 6b

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	551		600
B	(551) AAAAACTAAAAATAATTCTCCTGATTATATGAAATGACATTTTT		
A	(1) -----		CGCAATTTTT
Consensus	(551)		G ATTTTT
	601		650
B	(601) TGGAACATGAAGG-GTATTGATTTACACCTTTACACCT--TTCAAA		
A	(12) GTGAAGCTGAGGGAGGATTGGATTTACACCTATTCAAAAGTCATTCAAA		
Consensus	(601) GAA TGA GG G ATTG TTTAC C TT A A T TTCAAA		
	651		700
B	(648) G-----CCATTCAAGGATGAATATAGATTTGGCGATCAAACAC		
A	(62) GTTGTCCCTCCATTCAAGGATGAATGTAGATTTCAAGCATCAAACAC		
Consensus	(651) G CCATTCAAGGATGAAT TAGATTTT ATCAAACAC		
	701		750
B	(689) AAGAATCATTACGATAACATGCTTGGAACACACACATGCTTAAATTAAT		
A	(112) AAGAATCACTAGCATAACATGCTTGGAACACACACACACACACAC		
Consensus	(701) AAGAATCA TA ATAACATGCTTG AAC CACACA CTTAAATTAAT		
	751		800
B	(739) GGTGGAGTATCAAAT---TTTAAAT-ATTGTTGTCAAT-ACATACCC		
A	(160) GTAGGAATATCAAATCCAATATAAAATCATAGTTGTCAATTACATACTC		
Consensus	(751) G T GGA TATCAAAT T TAAAT AT GTTGTCAAT ACATAC C		
	801		850
B	(783) CGTCAATCTTCTTTTTACCAATAAACATTGAAATGTTGCTTCTTC		
A	(210) AATCAAGTCCCTTCTTACCAATAAACATCAACATATTGCTTCTTC		
Consensus	(801) TCAA CTTT TTTACCAATAAACAT A AT TTGCTTCTT C		
	851		900
B	(833) GTTAAGCATAAAAACATCAAAGTCTA-----GCAAAATGTTGTTTGC		
A	(260) ATTAAGCATAAAACATCAAAGTCTAAAGACTAGCAAAATGTTGTTTGC		
Consensus	(851) TTAAGCATA AAACATCAAAGTCTA GCAAAATGTTGTTTGC		
	901		950
B	(877) GATGACACATTCATA--TAGTTAAAGGATGCATGATTGATTACAAA		
A	(310) GATGACACATTCATACATAGTTAAAGATACTTGATTGATTACAAA		
Consensus	(901) GATGACACATTCATA TAGTTAAA GAT C TGATTGATTACAAA		
	951		1000
B	(925) ACAAAATACTAATAATTCTAGCACAAAGTTAAAGCAAGATTATAAGCT		
A	(360) AGAAATTACCAATAGTT-TAGCACAAAGTCTAAAGCATAATTA--AAGCA		
Consensus	(951) A AAA TAC AATA TT TAGCACAAAGT TAAAGCA ATTA AAGC		
	1001		1050
B	(975) TCATAGCATGTGGATATTCAATTGAAATATAGATTA-GATTGCCCTT		
A	(407) TCA---CATGTGCAGATTAT---GAAAAAAAGATTAAGATTGCCCTT		
Consensus	(1001) TCA CATGTG A ATT AT GAAA A AGATTA GATTGCCCTT		
	1051		1100
B	(1024) CATCACGGGTC---TAACAGCACCACTGTCACTACATGTCAAAAAA--TG		
A	(451) CATCACGGGTCGAATAATAGCACTACTGTCACTACATGTCAAAAAAATG		
Consensus	(1051) CATCACGGGTC TAA AGCAC ACTGTCACTACATGT AAAAAA TG		
	1101		1150
B	(1069) TCCTCTAGTACAGCACCGCTTTACTTGATTCCCTTGTCCATGCATGA		
A	(501) TCCTCTAGTACATCAAACCTTTCCATTGATTCCCTTATCC---ATGA		
Consensus	(1101) TCCTCTAGTAC A CA TTT TTGATTCCCTT TCC ATGA		
	1151		1200
B	(1119) AAAAAATCAAAACAATATGGACACACAAACTTGCCCCCCTTCC		
A	(547) AAAAAATAAACAAATTCTTAAGACACACAAAAAATGGCCCCACAT-CCTTT		
Consensus	(1151) AAAAAAT AA A A T TT GACACA AAA TG CCCCCAC T CCTTT		

Fig. 7a

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	1201	1250
B	(1169) TTCTTTCTGCCCTAGTTGTTGAGACTCATATTGATCAAATTGGCTAT	
A	(596) ---TTTCTGGCCTAGTTGTTGA-----	
Consensus	(1201) TTTCTG CCTAGTTGTTGA	
	1251	1300
B	(1219) GAATTCAAACAAAAATTCACTCTACCCATTGCATGTGT---GGGGCCCA	
A	(617) -----A---TTCATTCTAACTCTGAATATGTAACGAGGCCA	
Consensus	(1251) A TTCA TCTA C TTG AT TGT G GGCCCA	
	1301	1350
B	(1266) CATATAAATCCATGAAGGATTCAATGTCCATCCAAGTCAATGATTCAAC	
A	(652) C-TAAAAATCAAT-----CAATGATTAAAC	
Consensus	(1301) C TA AAATC AT CAATGATT AAC	
	1351	1400
B	(1316) ATATATAACATTGAATAATTAAATTCCAATTGCAGTATTATGATTAGA	
A	(676) ATAAAAAAA---TGAATAGTTAATTCCAATTGC-----	
Consensus	(1351) ATA A AA TGAATA TTTAATTCCAATTGC	
	1401	1450
B	(1366) TTGATTGCTGCAAATACGGTCCGTGAATGTGATCACTCACGAGAAAGAGGT	
A	(707) -----TGCAACATGGTCCGTGAATATGA---CTCACGAGAAAGATAT	
Consensus	(1401) TGCAA A GGTCCGTGAAT TGA CTCACGAGAAAGA T	
	1451	1500
B	(1416) ATCAAAATTCAAGGTATTTATTATTAAACAAATAAAATTCAAGG	
A	(746) ATCAAAATATCAA-----AATTTCATAG	
Consensus	(1451) ATCAAAAT TCAA AATTTCAG G	
	1501	1550
B	(1466) TCTTGTCAACCATAAACCTCCTCACTCACACCCAATTCTCTTAAGTGT	
A	(769) TTTTTTCACCATATAAACCTCATCACTCATTC--TATTTTTTAAGTGC	
Consensus	(1501) T TT TTCACCATATAAACCTC TCACTCA C ATT T TTAAGTG	
	1551	1600
B	(1516) ATGACTTCATAGTAC--ACTACACTACTTCTTGAAACATGGCTAACTA	
A	(817) AAAGCTTCATAGTAGTGAGCACACACATTACACTAAAATCTCGAAACTT	
Consensus	(1551) A CTTCATAGTA A ACAC TT C T AAA T AACT	
	1601	1650
B	(1564) TGCTCTAGCCAATGTTTCATCCTCTTGAACTTGAGTACCTTACTCA	
A	(867) A-----	
Consensus	(1601)	

Fig. 7b

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	1	50
SEQ ID NO: 9	(1)	---
SEQ ID NO: 8	(1)	AAGCTTTCAACAATCATGCCCATGTCAAGTGTAAAACAGGTTACCTCT
SEQ ID NO: 7	(1)	AAGCTTTCAACAATCATGCCCATGTCAAGTGTAAAACAGGTTACCTCT
Consensus	(1)	AAGCTTTCAACAATCATGCCCATGTCAAGTGTAAAACAGGTTACCTCT
		51
SEQ ID NO: 9	(48)	CTTAAATAACCGTATTAAAATGCTGAATGATGTATATATGTGGGTTCAAA
SEQ ID NO: 8	(51)	CTTAAATAACCGTATTAAAATGCTGAATGATGTATATATGTGGGTTCAAA
SEQ ID NO: 7	(51)	CTTAAATAACCGTATTAAAATGCTGAATGATGTATATATGTGGGTTCAAA
Consensus	(51)	CTTAAATAACCGTATTAAAATGCTGAATGATGTATATATGTGGGTTCAAA
		100
SEQ ID NO: 9	(98)	TTACATAATTGTAAGTATGTTACACATTGTATAAATATGTTTAGAGAA
SEQ ID NO: 8	(101)	TTACATAATTGTAAGTATGTTACACATTGTATAAATATGTTTAGAGAA
SEQ ID NO: 7	(101)	TTACATAATTGTAAGTATGTTACACATTGTATAAATATGTTTAGAGAA
Consensus	(101)	TTACATAATTGTAAGTATGTTACACATTGTATAAATATGTTTAGAGAA
		150
SEQ ID NO: 9	(148)	AAATGTAAACTTATATGTCTAAAGTTATAAAAGAAACATGTCCAACACAT
SEQ ID NO: 8	(151)	AAATGTAAACTTATATGTCTAAAGTTATAAAAGAAACATGTCCAACACAT
SEQ ID NO: 7	(151)	AAATGTAAACTTATATGTCTAAAGTTATAAAAGAAACATGTCCAACACAT
Consensus	(151)	AAATGTAAACTTATATGTCTAAAGTTATAAAAGAAACATGTCCAACACAT
		200
SEQ ID NO: 9	(198)	TTCAGTTAAGATTTAAATAGTATAAATTAAAAATTATCGATGATGACAAA
SEQ ID NO: 8	(201)	TTCAGTTAAGATTTAAATAGTATAAATTAAAAATTATCGATGATGACAAA
SEQ ID NO: 7	(201)	TTCAGTTAAGATTTAAATAGTATAA-TTAAAAATTATCGATGATGACAAA
Consensus	(201)	TTCAGTTAAGATTTAAATAGTATAAATTAAAAATTATCGATGATGACAAA
		250
SEQ ID NO: 9	(248)	AAATTGTAAATATAATTCACTTTAAAAAAAGTTAAGAAATTGAAAAAGGA
SEQ ID NO: 8	(251)	AAATTGTAAATATAATTCACTTTAAAAAAAGTTAAGAAATTGAAAAAGGA
SEQ ID NO: 7	(250)	AAATTGTAAATATAATTCACTTTAAAAAAAGTTAAGAAATTGAAAAAGGA
Consensus	(251)	AAATTGTAAATATAATTCACTTTAAAAAAAGTTAAGAAATTGAAAAAGGA
		300
SEQ ID NO: 9	(298)	AATATCGAGAAAAAAATATGTCGATTATATATATGTGTGAGCTGAGTGAA
SEQ ID NO: 8	(301)	AATATCGAGAAAAAAATATGTCGATTATATATATGTGTGAGCTGAGTGAA
SEQ ID NO: 7	(300)	AATATCGAGAAAAAAATATGTCGATTATATATATGTGTGAGCTGAGTGAA
Consensus	(301)	AATATCGAGAAAAAAATATGTCGATTATATATGTGTGAGCTGAGTGAA
		350
SEQ ID NO: 9	(348)	TATATATGTATATTTATTTGACTGAATATATGTGTGTATAGACAATA
SEQ ID NO: 8	(351)	TATATATGTATATTTATTTGACTGAATATATGTGTGTATAGACAATA
SEQ ID NO: 7	(350)	TATATATGTATATTTATTTGACTGAATATATGTGTGTATAGACAATA
Consensus	(351)	TATATATGTATATTTATTTGACTGAATATATGTGTGTATAGACAATA
		400
SEQ ID NO: 9	(398)	ATGCGCAGAATGCCGATCGATGAATTGTTACTGCATTTCAAATATGTG
SEQ ID NO: 8	(401)	ATGCGCAGAATGCCGATCGATGAATTGTTACTGCATTTCAAATATGTG
SEQ ID NO: 7	(400)	ATGCGCAGAATGCCGATCGATGAATTGTTACTGCATTTCAAATATGTG
Consensus	(401)	ATGCGCAGAATGCCGATCGATGAATTGTTACTGCATTTCAAATATGTG
		450
SEQ ID NO: 9	(448)	TGCATAAGCGTTCACATGTCACCCATGTTGAATTAGTTCTTCCCTGG
SEQ ID NO: 8	(451)	TGCATAAGCGTTCACATGTCACCCATGTTGAATTAGTTCTTCCCTGG
SEQ ID NO: 7	(450)	TGCATAAGCGTTCACATGTCACCCATGTTGAATTAGTTCTTCCCTGG
Consensus	(451)	TGCATAAGCGTTCACATGTCACCCATGTTGAATTAGTTCTTCCCTGG
		500
SEQ ID NO: 9	(448)	
SEQ ID NO: 8	(451)	
SEQ ID NO: 7	(450)	
Consensus	(451)	
		550

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SEQ ID NO: 9 (498) ATGAATTACTAAGAACAGATTGATTGATAGTACTATATTAAATTATGTA  
SEQ ID NO: 8 (501) ATGAATTACTAAGAACAGATTGATTGATAGTACTATATTAAATTATGTA  
SEQ ID NO: 7 (500) ATGAATTACTAAGAACAGATTGATTGATAGTACTATATTAAATTATGTA  
Consensus (501) ATGAATTACTAAGAACAGATTGATTGATAGTACTATATTAAATTATGTA  
551 600  
SEQ ID NO: 9 (548) GCTTTACATGTCAGGAAAATGTAGTTGCAGTATTATGTAATGTAATTAAT  
SEQ ID NO: 8 (551) GCTTTACATGTCAGGAAAATGTAGTTGCAGTATTATGTAATGTAATTAAT  
SEQ ID NO: 7 (550) GCTTTACATGTCAGGAAAATGTAGTTGCAGTATTATGTAATGTAATTAAT  
Consensus (551) GCTTTACATGTCAGGAAAATGTAGTTGCAGTATTATGTAATGTAATTAAT  
601 650  
SEQ ID NO: 9 (598) AGGAAGTCACAGACAATTGAAAGACAATTCTTAGCTTACCTATCTCAT  
SEQ ID NO: 8 (601) AGGAAGTCACAGACAATTGAAAGACAATTCTTAGCTTACCTATCTCAT  
SEQ ID NO: 7 (600) AGGAAGTCACAGACAATTGAAAGACAATTCTTAGCTTACCTATCTCAT  
Consensus (601) AGGAAGTCACAGACAATTGAAAGACAATTCTTAGCTTACCTATCTCAT  
651 700  
SEQ ID NO: 9 (648) GCCACAAATTATGTAACGACAGTAAAATGTTAAAAGCAAAA-----  
SEQ ID NO: 8 (651) GCCACAAATTATGTAACGACAGTAAAATGTTAAAAGCAAAA-----  
SEQ ID NO: 7 (650) GCCACAAATTATGTAACGACAGTAAAATGTTAAAAGCAAAAAGCAAAA  
Consensus (651) GCCACAAATTATGTAACGACAGTAAAATGTTAAAAGCAAAA  
701 750  
SEQ ID NO: 9 (692) AAAAGAAAGAAGAAGAAGTAATAAATGAAATTATAGAATGTAAC  
SEQ ID NO: 8 (695) AAAAGAAAGAAGAAGAAGTAATAAATGAAATTATAGAATGTAAC  
SEQ ID NO: 7 (700) AAAAGAAAGAAGAAGAAGTAATAAATGAAATTATAGAATGTAAC  
Consensus (701) AAAAGAAAGAAGAAGAAGTAATAAATGAAATTATAGAATGTAAC  
751 800  
SEQ ID NO: 9 (742) TTTGTCTCATCTGCCCTATAATTCTGCAGCAGCCAAAGCATAATAGCA  
SEQ ID NO: 8 (745) TTTGTCTCATCTGCCCTATAATTCTGCAGCAGCCAAAGCATAATAGCA  
SEQ ID NO: 7 (750) TTTGTCTCATCTGCCCTATAATTCTGCAGCAGCCAAAGCATAATAGCA  
Consensus (751) TTTGTCTCATCTGCCCTATAATTCTGCAGCAGCCAAAGCATAATAGCA  
801 850  
SEQ ID NO: 9 (792) TGCAATATGCACATATTGTTAGGCTTTAGCCTCCACGATCTGTTAA  
SEQ ID NO: 8 (795) TGCAATATGCACATATTGTTAGGCTTTAGCCTCCACGATCTGTTAA  
SEQ ID NO: 7 (800) TGCAATATGCACATATTGTTAGGCTTTAGC-TCCACGATCTGTTAA  
Consensus (801) TGCAATATGCACATATTGTTAGGCTTTAGCCTCCACGATCTGTTAA  
851 900  
SEQ ID NO: 9 (842) TGGAAAGTAAAAAGTAAGAGATATGAAGATTCAATTGGCAGCCATGGTCC  
SEQ ID NO: 8 (845) TGGAAAGTAAAAAGTAAGAGATATGAAGATTCAATTGGCAGCCATGGTCC  
SEQ ID NO: 7 (849) TGGAAAGTAAAAAGTAAGAGATATGAAGATTCAATTGGCAGCCATGGTCC  
Consensus (851) TGGAAAGTAAAAAGTAAGAGATATGAAGATTCAATTGGCAGCCATGGTCC  
901 950  
SEQ ID NO: 9 (892) CAGGGAAAGCACTAGAACGATATGAAATGACATAAAAGGTACCATGCATAA  
SEQ ID NO: 8 (895) CAGGGAAAGCACTAGAACGATATGAAATGACATAAAAGGTACCATGCATAA  
SEQ ID NO: 7 (899) CAGGGAAAGCACTAGAACGATATGAAATGAC-TAAAAGGTACCATGCATAA  
Consensus (901) CAGGGAAAGCACTAGAACGATATGAAATGACATAAAAGGTACCATGCATAA  
951 1000  
SEQ ID NO: 9 (942) TGCTTTAAATGCTGCTATAGAATCAAAAATGAAGAGATGTGACAAATT  
SEQ ID NO: 8 (945) TGCTTTAAATGCTGCTATAGAATCAAAAATGAAGAGATGTGACAAATT  
SEQ ID NO: 7 (948) TGCTTTAAATGCTGCTATAGAATCAAAAATGAAGAGATGTGACAAATT  
Consensus (951) TGCTTTAAATGCTGCTATAGAATCAAAAATGAAGAGATGTGACAAATT

Fig. 8b

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	1001	1050
SEQ ID NO: 9 (992)	GTTACATCTAATACGCAATAATTGACAAAGACGACTATGCCTTATATA	
SEQ ID NO: 8 (995)	GTTACATCTAATACGCAATAATTGACAAAGACGACTATGCCTTATATA	
SEQ ID NO: 7 (998)	GTTACATCTAATACGCAATAATTGACAAAGACGACTATGCCTTATATA	
Consensus (1001)	GTTACATCTAATACGCAATAATTGACAAAGACGACTATGCCTTATATA	
	1051	1100
SEQ ID NO: 9 (1042)	TTTATTTAATTAGTTGGCGTCTCTTATTATAAAGAAAATAAGGGCAGTG	
SEQ ID NO: 8 (1045)	TTTATTTAATTAGTTGGCGTCTCTTATTATAAAGAAAATAAGGGCAGTG	
SEQ ID NO: 7 (1048)	TTTATTTAATTAGTTGGCGTCTCTTATTATAAAGAAAATAAGGGCAGTG	
Consensus (1051)	TTTATTTAATTAGTTGGCGTCTCTTATTATAAAGAAAATAAGGGCAGTG	
	1101	1150
SEQ ID NO: 9 (1092)	TCAACATTCAGGCAACTAGTTAGTTATTTATTTCTTGTATATAATT	
SEQ ID NO: 8 (1095)	TCAACATTCAGGCAACTAGTTAGTTATTTATTTCTTGTATATAATT	
SEQ ID NO: 7 (1098)	TCAACATTCAGGCAACTAGTTAGTTATTTATTTCTTGTATATAATT	
Consensus (1101)	TCAACATTCAGGCAACTAGTTAGTTATTTATTTCTTGTATATAATT	
	1151	1200
SEQ ID NO: 9 (1142)	ATTCCATATAGCTAGCTGTCTCTATCTAATCCAAATCCGCTTCCACAA	
SEQ ID NO: 8 (1145)	ATTCCATATAGCTAGCTGTCTCTATCTAATCCAAATCCGCTTCCACAA	
SEQ ID NO: 7 (1148)	ATTCCATATAGCTAGCTGTCTCTATCTAATCCAAATCCGCTTCCACAA	
Consensus (1151)	ATTCCATATAGCTAGCTGTCTCTATCTAATCCAAATCCGCTTCCACAA	
	1201	1250
SEQ ID NO: 9 (1192)	CCAACTTGGTCGCATTGGTCAAAAAACTCAATATCAATATTTCGAAAT	
SEQ ID NO: 8 (1195)	CCAACTTGGTCGCATTGGTCAAAAAACTCAATATCAATATTTCGAAAT	
SEQ ID NO: 7 (1198)	CCAACTTGGT-----CCAAAAACTCAATATCAATATTTCAAAT	
Consensus (1201)	CCAACTTGGTCGCATTGGTCAAAAAACTCAATATCAATATTTCGAAAT	
	1251	1300
SEQ ID NO: 9 (1242)	AGTTTAGCATTGTTAGGAAGAGAATTGTAAGAGATAAAATCTAAGTAC	
SEQ ID NO: 8 (1245)	AGTTTAGCATTGTTAGGAAGAGAATTGTAAGAGATAAAATCTAAGTAC	
SEQ ID NO: 7 (1239)	AGTTTAGCATTGTTAGGAAGAGAATTGTAAGAGATAAAATCTAAGTAC	
Consensus (1251)	AGTTTAGCATTGTTAGGAAGAGAATTGTAAGAGATAAAATCTAAGTAC	
	1301	1350
SEQ ID NO: 9 (1292)	TCCACCTACCAAGATAAAATAGTTGGATAATGGTAAAAAGTTGTAT	
SEQ ID NO: 8 (1295)	TCCACCTACCAAGATAAAATAGTTGGATAATGGTAAAAAGTTGTAT	
SEQ ID NO: 7 (1289)	TCCACCTACCAAGATAAAATAGTTGGATAATGGTAAAAA-GTTGTAT	
Consensus (1301)	TCCACCTACCAAGATAAAATAGTTGGATAATGGTAAAAAGTTGTAT	
	1351	1393
SEQ ID NO: 9 (1342)	AAAGGGCAACACTACCTCTCCTAATGGCAGTA-----	
SEQ ID NO: 8 (1345)	AAAGGGCAACACTACCTCTCCTAATGGCAGTACCAAAACCAAG	
SEQ ID NO: 7 (1338)	AAAGGGCAACACTACCTCTCCTAATGGCAGTACCAAAACCAAG	
Consensus (1351)	AAAGGGCAACACTACCTCTCCTAATGGCAGTACCAAAACCAAG	

Fig. 8c

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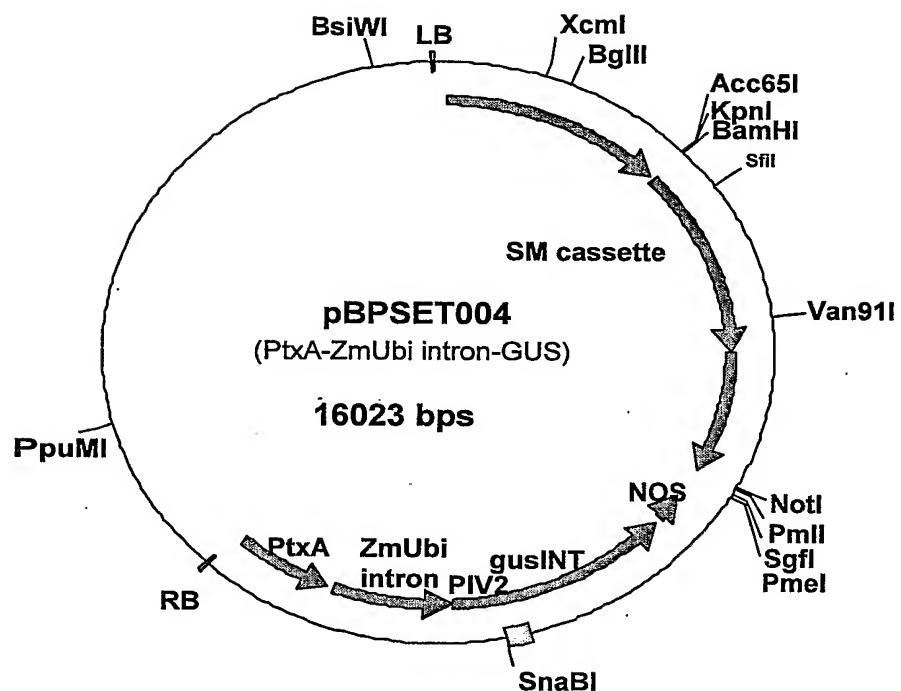


Fig. 9